



## SEQUENCE LISTING

<110> Aventis Pasteur Limited

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

<130> 77813-6

10 <140> PCT/CA99/01224

<141> 1999-12-22

<150> US 60/114,060

<151> 1998-12-28

<150> US 60/123,967

<151> 1999-03-12

20 <150> US 60/141,271

<151> 1999-06-30

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 1637

<212> DNA

30 <213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (51)..(1595)

<400> 1

gaaataaaaa actatcagaa tagaaaaataa aagtatttca gagggtaa atg aca 56  
Met Thr  
1

40 aaa acc gaa gaa aaa cct ttt gga aaa ttg cgc tct ttc ttg tgg ccg 104  
Lys Thr Glu Glu Lys Pro Phe Gly Lys Leu Arg Ser Phe Leu Trp Pro  
5 10 15

ata cat act cac gag cta aag aaa gtt ctg cca atg ttc cta atg ttc 152  
Ile His Thr His Glu Leu Lys Lys Val Leu Pro Met Phe Leu Met Phe  
20 25 30

50 ttc tgt att aca ttt aac tat acg gtg tta cgc gat aca aaa gac act 200  
Phe Cys Ile Thr Phe Asn Tyr Thr Val Leu Arg Asp Thr Lys Asp Thr  
35 40 45 50

ctt att gtg gga gct cct ggt tct ggt gca gag gca ata cct ttc atc 248  
Leu Ile Val Gly Ala Pro Gly Ser Gly Ala Glu Ala Ile Pro Phe Ile  
55 60 65

	aag	ttt	tgg	ctt	gtt	gtc	ccc	tgt	gct	att	atc	ttt	atg	ctt	att	tat	296
	Lys	Phe	Trp	Leu	Val	Val	Pro	Cys	Ala	Ile	Ile	Phe	Met	Leu	Ile	Tyr	
				70					75					80			
	gca	aag	cta	agt	aat	att	tta	agt	aag	cag	gcc	tta	ttt	tat	gca	gtg	344
	Ala	Lys	Leu	Ser	Asn	Ile	Leu	Ser	Lys	Gln	Ala	Leu	Phe	Tyr	Ala	Val	
			85					90					95				
10	gga	acg	ccc	ttt	tta	att	ttc	ttt	gcc	ctg	ttc	ccg	act	gta	att	tat	392
	Gly	Thr	Pro	Phe	Leu	Ile	Phe	Phe	Ala	Leu	Phe	Pro	Thr	Val	Ile	Tyr	
		100					105					110					
	ccg	cta	cgc	gat	gtt	tta	cat	cct	aca	gaa	ttt	gct	gac	cgt	tta	cag	440
	Pro	Leu	Arg	Asp	Val	Leu	His	Pro	Thr	Glu	Phe	Ala	Asp	Arg	Leu	Gln	
	115					120					125					130	
	gcc	atc	cta	cct	cca	gga	ttg	cta	gga	ctc	gtt	gcc	atc	tta	aga	aac	488
	Ala	Ile	Leu	Pro	Pro	Gly	Leu	Leu	Gly	Leu	Val	Ala	Ile	Leu	Arg	Asn	
				135					140						145		
20	tgg	aca	ttt	gct	gca	ttt	tat	gta	ctt	gct	gaa	cta	tgg	gga	agc	gtc	536
	Trp	Thr	Phe	Ala	Ala	Phe	Tyr	Val	Leu	Ala	Glu	Leu	Trp	Gly	Ser	Val	
			150					155					160				
	atg	cta	tct	cta	atg	ttc	tgg	gga	ttt	gct	aat	gaa	att	aca	aaa	atc	584
	Met	Leu	Ser	Leu	Met	Phe	Trp	Gly	Phe	Ala	Asn	Glu	Ile	Thr	Lys	Ile	
			165				170					175					
30	cac	gaa	gca	aag	cgt	ttc	tac	gct	ctt	ttc	ggt	atc	gga	gct	aat	att	632
	His	Glu	Ala	Lys	Arg	Phe	Tyr	Ala	Leu	Phe	Gly	Ile	Gly	Ala	Asn	Ile	
		180					185					190					
	tct	tta	cta	gct	tct	ggt	cgt	gca	att	gtt	tgg	gct	tca	aag	ttg	aga	680
	Ser	Leu	Leu	Ala	Ser	Gly	Arg	Ala	Ile	Val	Trp	Ala	Ser	Lys	Leu	Arg	
	195					200					205					210	
	gct	tcc	gtt	tct	gaa	ggt	gta	gat	cct	tgg	gga	att	tct	tta	cgt	ctt	728
	Ala	Ser	Val	Ser	Glu	Gly	Val	Asp	Pro	Trp	Gly	Ile	Ser	Leu	Arg	Leu	
				215					220						225		
40	ttg	atg	gct	atg	act	att	gta	tct	gga	ctt	gtt	ctt	atg	gcc	agt	tac	776
	Leu	Met	Ala	Met	Thr	Ile	Val	Ser	Gly	Leu	Val	Leu	Met	Ala	Ser	Tyr	
				230				235						240			
	tgg	tgg	atc	aat	aag	aac	gta	ttg	acc	gat	cct	cgc	ttc	tat	aat	cca	824
	Trp	Trp	Ile	Asn	Lys	Asn	Val	Leu	Thr	Asp	Pro	Arg	Phe	Tyr	Asn	Pro	
			245					250					255				
50	gaa	gaa	atg	caa	aag	ggg	aaa	aaa	ggt	gct	aaa	cct	aaa	atg	aat	atg	872
	Glu	Glu	Met	Gln	Lys	Gly	Lys	Lys	Gly	Ala	Lys	Pro	Lys	Met	Asn	Met	
		260					265					270					
	aaa	gat	agc	ttc	ctc	tat	ctt	gat	aga	tct	cct	tat	att	ctt	tta	tta	920
	Lys	Asp	Ser	Phe	Leu	Tyr	Leu	Asp	Arg	Ser	Pro	Tyr	Ile	Leu	Leu	Leu	
		275				280					285					290	

	act ctc ttg gtt att gcc tat ggt att tgc att aac tta atc gaa gtg	968
	Thr Leu Leu Val Ile Ala Tyr Gly Ile Cys Ile Asn Leu Ile Glu Val	
	295 300 305	
	act tgg aaa agt cag ctg aaa ctg caa tat cct aat atg aat gac tat	1016
	Thr Trp Lys Ser Gln Leu Lys Leu Gln Tyr Pro Asn Met Asn Asp Tyr	
	310 315 320	
10	agt gag ttc atg ggg aac ttc tcc ttc tgg act ggc gta gta tcc gta	1064
	Ser Glu Phe Met Gly Asn Phe Ser Phe Trp Thr Gly Val Val Ser Val	
	325 330 335	
	ctt atc atg cta ttt gtt ggt ggt aac gtc att cgt aaa ttt gga tgg	1112
	Leu Ile Met Leu Phe Val Gly Gly Asn Val Ile Arg Lys Phe Gly Trp	
	340 345 350	
20	tta act gga gcc cta gtc act cct gtc atg gtt ctc cta aca ggt atc	1160
	Leu Thr Gly Ala Leu Val Thr Pro Val Met Val Leu Leu Thr Gly Ile	
	355 360 365 370	
	gtt ttc ttc gct ctt gtt atc ttt aga aac caa gct tct ggg ctg gtc	1208
	Val Phe Phe Ala Leu Val Ile Phe Arg Asn Gln Ala Ser Gly Leu Val	
	375 380 385	
	gct atg ttc ggt aca act cct ctc atg cta gct gtg gtt gtc gga gct	1256
	Ala Met Phe Gly Thr Thr Pro Leu Met Leu Ala Val Val Val Gly Ala	
	390 395 400	
30	ata cag aat att ctt tcg aaa tcc aca aaa tac gct ctc ttt gac tca	1304
	Ile Gln Asn Ile Leu Ser Lys Ser Thr Lys Tyr Ala Leu Phe Asp Ser	
	405 410 415	
	act aaa gaa atg gcc tat atc cct ctt gac caa gag caa aaa gtc aaa	1352
	Thr Lys Glu Met Ala Tyr Ile Pro Leu Asp Gln Glu Gln Lys Val Lys	
	420 425 430	
40	ggt aag gct gct att gat gta gtt gcc gcc cgc ttc gga aaa tca gga	1400
	Gly Lys Ala Ala Ile Asp Val Val Ala Ala Arg Phe Gly Lys Ser Gly	
	435 440 445 450	
	gga gct tta atc caa caa ggt ttg ctc gtt atc tgt gga agt att gga	1448
	Gly Ala Leu Ile Gln Gln Gly Leu Leu Val Ile Cys Gly Ser Ile Gly	
	455 460 465	
	gct atg acc cct tat ctt gca gtg att ctt ctt ttc atc att gct att	1496
	Ala Met Thr Pro Tyr Leu Ala Val Ile Leu Leu Phe Ile Ile Ala Ile	
	470 475 480	
50	tgg ttg gtt tct gca act aag tta aac aaa cta ttc tta gcg cag tct	1544
	Trp Leu Val Ser Ala Thr Lys Leu Asn Lys Leu Phe Leu Ala Gln Ser	
	485 490 495	
	gct ctt aaa gaa caa gaa gtg gct caa gaa gat tca gct cct gct tct	1592
	Ala Leu Lys Glu Gln Glu Val Ala Gln Glu Asp Ser Ala Pro Ala Ser	
	500 505 510	

tca tagagttgct tctcttactc ttgttgatcc ctacctgctt tt

1637

Ser

515

&lt;210&gt; 2

&lt;211&gt; 515

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

10

&lt;400&gt; 2

Met	Thr	Lys	Thr	Glu	Glu	Lys	Pro	Phe	Gly	Lys	Leu	Arg	Ser	Phe	Leu
1				5					10					15	

Trp	Pro	Ile	His	Thr	His	Glu	Leu	Lys	Lys	Val	Leu	Pro	Met	Phe	Leu
			20					25					30		

Met	Phe	Phe	Cys	Ile	Thr	Phe	Asn	Tyr	Thr	Val	Leu	Arg	Asp	Thr	Lys
		35					40					45			

20

Asp	Thr	Leu	Ile	Val	Gly	Ala	Pro	Gly	Ser	Gly	Ala	Glu	Ala	Ile	Pro
	50					55					60				

Phe	Ile	Lys	Phe	Trp	Leu	Val	Val	Pro	Cys	Ala	Ile	Ile	Phe	Met	Leu
65					70					75					80

Ile	Tyr	Ala	Lys	Leu	Ser	Asn	Ile	Leu	Ser	Lys	Gln	Ala	Leu	Phe	Tyr
				85					90					95	

30

Ala	Val	Gly	Thr	Pro	Phe	Leu	Ile	Phe	Phe	Ala	Leu	Phe	Pro	Thr	Val
			100					105					110		

Ile	Tyr	Pro	Leu	Arg	Asp	Val	Leu	His	Pro	Thr	Glu	Phe	Ala	Asp	Arg
		115					120					125			

Leu	Gln	Ala	Ile	Leu	Pro	Pro	Gly	Leu	Leu	Gly	Leu	Val	Ala	Ile	Leu
	130					135					140				

40

Arg	Asn	Trp	Thr	Phe	Ala	Ala	Phe	Tyr	Val	Leu	Ala	Glu	Leu	Trp	Gly
145				150						155					160

Ser	Val	Met	Leu	Ser	Leu	Met	Phe	Trp	Gly	Phe	Ala	Asn	Glu	Ile	Thr
			165						170					175	

Lys	Ile	His	Glu	Ala	Lys	Arg	Phe	Tyr	Ala	Leu	Phe	Gly	Ile	Gly	Ala
		180						185					190		

Asn	Ile	Ser	Leu	Leu	Ala	Ser	Gly	Arg	Ala	Ile	Val	Trp	Ala	Ser	Lys
		195					200					205			

50

Leu	Arg	Ala	Ser	Val	Ser	Glu	Gly	Val	Asp	Pro	Trp	Gly	Ile	Ser	Leu
	210					215					220				

Arg	Leu	Leu	Met	Ala	Met	Thr	Ile	Val	Ser	Gly	Leu	Val	Leu	Met	Ala
225					230					235					240

Ser	Tyr	Trp	Trp	Ile	Asn	Lys	Asn	Val	Leu	Thr	Asp	Pro	Arg	Phe	Tyr
				245					250					255	

	Asn	Pro	Glu	Glu	Met	Gln	Lys	Gly	Lys	Lys	Gly	Ala	Lys	Pro	Lys	Met
				260					265					270		
	Asn	Met	Lys	Asp	Ser	Phe	Leu	Tyr	Leu	Asp	Arg	Ser	Pro	Tyr	Ile	Leu
		275						280					285			
	Leu	Leu	Thr	Leu	Leu	Val	Ile	Ala	Tyr	Gly	Ile	Cys	Ile	Asn	Leu	Ile
		290					295					300				
10	Glu	Val	Thr	Trp	Lys	Ser	Gln	Leu	Lys	Leu	Gln	Tyr	Pro	Asn	Met	Asn
	305					310					315					320
	Asp	Tyr	Ser	Glu	Phe	Met	Gly	Asn	Phe	Ser	Phe	Trp	Thr	Gly	Val	Val
					325					330					335	
	Ser	Val	Leu	Ile	Met	Leu	Phe	Val	Gly	Gly	Asn	Val	Ile	Arg	Lys	Phe
				340					345					350		
20	Gly	Trp	Leu	Thr	Gly	Ala	Leu	Val	Thr	Pro	Val	Met	Val	Leu	Leu	Thr
		355						360					365			
	Gly	Ile	Val	Phe	Phe	Ala	Leu	Val	Ile	Phe	Arg	Asn	Gln	Ala	Ser	Gly
		370					375					380				
	Leu	Val	Ala	Met	Phe	Gly	Thr	Thr	Pro	Leu	Met	Leu	Ala	Val	Val	Val
	385					390					395					400
30	Gly	Ala	Ile	Gln	Asn	Ile	Leu	Ser	Lys	Ser	Thr	Lys	Tyr	Ala	Leu	Phe
					405					410					415	
	Asp	Ser	Thr	Lys	Glu	Met	Ala	Tyr	Ile	Pro	Leu	Asp	Gln	Glu	Gln	Lys
				420					425					430		
	Val	Lys	Gly	Lys	Ala	Ala	Ile	Asp	Val	Val	Ala	Ala	Arg	Phe	Gly	Lys
			435					440					445			
	Ser	Gly	Gly	Ala	Leu	Ile	Gln	Gln	Gly	Leu	Leu	Val	Ile	Cys	Gly	Ser
		450					455					460				
40	Ile	Gly	Ala	Met	Thr	Pro	Tyr	Leu	Ala	Val	Ile	Leu	Leu	Phe	Ile	Ile
	465					470					475					480
	Ala	Ile	Trp	Leu	Val	Ser	Ala	Thr	Lys	Leu	Asn	Lys	Leu	Phe	Leu	Ala
					485					490					495	
	Gln	Ser	Ala	Leu	Lys	Glu	Gln	Glu	Val	Ala	Gln	Glu	Asp	Ser	Ala	Pro
				500					505					510		
50	Ala	Ser	Ser													
			515													

&lt;210&gt; 3

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; 5' PCR primer

&lt;400&gt; 3

ataagaatgc ggccgccacc atgacaaaaa ccgaagaaaa acc

43

&lt;210&gt; 4

&lt;211&gt; 29

10

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; 3' PCR primer

&lt;400&gt; 4

gcgccgatc cctgaagaag caggagctg

29